

GehCore Version 4.3  
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Run on : November 20, 2000, 14:05:12 ; Search time 14.9 Seconds  
(without alignments)  
668.675 Million cell updates/sec

Little: 55 55 55 55 55  
 Perfect score: 808 808 808 808 808  
 Sequence: 1 NGRLHCTTAVIRNINDQVL.....KKDENGDKSVMFTLTNLHQ S 157  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of sites satisfying these criteria:

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summa

Da

1:  
2:  
3:  
4:  
pi  
pi  
pi  
pi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
8	100	100%	100	1	DB1

cytokine IGIF -  
endopeptidase La

interleukin-1 beta hypothetical protein interleukin-1 beta hypothetical protein interleukin-1 beta

*hypothetical protein*, cell division control, hypothetical protein, toxin, nontoxic

botulinum neurotoxin  
hypothetical protein  
hypothetical protein

interleukin-1 beta hypothetical protein hypothetical protein character and has

characteristic and unique hypothetical protein  
probable protein EIN2 - A

hypothetical protein, interleukin-1 alpha, hypothetical protein, C64401

hypothetical AIP carboxy-terminal probable lipoxigenase interleukin-1 beta

26 73 3.3 200 1 323010  
27 75 9.3 621 2 A71961  
28 75 9.3 624 2 S67382  
29 75 9.3 1146 2 E70204

ALIGNMENT

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RESULT          1
S60226
cytokine IGIF - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C;Accession: S60226
R;Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig
A;Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A;Reference number: S60226; MUID:96061009
A;Accession: S60226
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-192 <OKA>
A;Cross-references: EMBL:D49949; NID:91064822; PIDN:BAA08705.1; PID:91064823
C;Superfamily: Mus musculus cytokine IGIF

Query Match          99.8%; Score 806; DB 2; Length 192;
Best Local Similarity 99.4%; Pred. No. 1.9e-65;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          1 NFGRHLHCTTAVIRININDQVLFVDKRQQPVFEDMTDIDQSASEPOTRLIIMYKDSEVRGLA 60
Db          36 NFGRHLHCTTAVIRININDQVLFVDKRQQPVFEDMTDIDQSASEPOTRLIIMYKDSEVRGLA 95
QY          61 VTLSVKDSKXSTLSCKNKTLISFEEMDPHENIDDIOQSDLIFFQKRVPHNKFEESSLYEG 120
Db          96 VTLSVKDSKMSLTLSCKNKTLISFEEMDPHENIDDIOQSDLIFFQKRVPHNKFEESSLYEG 155
QY          121 HFLACQKEDDAFKLILKKKDENGDKSVMFLLTNLHQ 157
Db          156 HFLACQKEDDAFKLILKKKDENGDKSVMFLLTNLHQ 192

RESULT          2
A64070
endopeptidase La (EC 3.4.21.53) - Haemophilus influenzae (strain Rd KW20)
N;Alternate names: ATP-dependent proteinase Ion; ATP-dependent serine proteinase La
N;Contains: adenosinetriphosphatase (EC 3.6.1.3)
C;Species: Haemophilus influenzae
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 18-Jun-1999
C;Accession: A64070
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkinis, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630
A;Accession: A64070

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A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-803 <TIGR>  
A;Cross-references: GB:U32729; GB:L42023; NID:g1573439; PIDN: AAC22121.1; PID:g1573440; T  
C;Comment: This allosteric enzyme catalyzes the hydrolysis of large proteins in the pres  
C;Genetics:  
A;Gene: Ion, ion-A  
C;Superfamily: ATP-dependent serine proteinase La  
C;Keywords: allosteric regulation; ATP; DNA binding; heat shock; hydrolase; P-loop; seri  
F;356-363/Region: nucleotide-binding motif A (P-loop)  
F;419-424/Region: nucleotide-binding motif B  
F;679/Active site: Ser #status predicted

Query Match 10.2%; Score 82.5; DB 1; Length 803;  
Best Local Similarity 18.9%; Pred. No. 10; Mismatches 71; Indels 85; Gaps 7;  
Matches 44; Conservative 33; Mismatches 71; Indels 85; Gaps 7;

Qy 3 GRLHCTTAVIRNIND--QWLFVDKR----QPVFEDMTDIDQSAS----- 40  
Db 30 GRAKSINALEAMNDKQILLVSQREADLEEPPEPDLFDVGTIANIQQLKLPPDTVKVL 89

Qy 41 -EPOTRLIIMYKDE-----VRGLAVTLSVKDSKXSTLSCKNKIISFE 83  
Db 90 VEGONRAKINSLEDGEKCFSAQITPIETTYGDEKELVWAKSAVLSEFENWLTINKKVPTD 149

Qy 84 EMDPPENTDDI-----QSDLIFFQK 103  
Db 150 ILNALQRIDDVDRLLADTMMAHLPVSVRHKQNLAELANVQERLEYLLGMNESEADILQVEK 209

Qy 104 RVPGHNKMEFESSLYVEGHFLACQKEDDAFKLILKKDDENGDKSVMFTLTNLHQ 156  
Db 210 RIRGRVKKQMEKS-QRNYYL----NEQIKAIRKEMDGGENEDTIDEVEOLHQ 256

RESULT 3

JN0724 interleukin-1 beta precursor - pig  
N;Alternate names: hematopoietin-1; IL-1 beta  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 14-Jul-1994 #sequence\_revision 22-Nov-1996 #text\_change 22-Jun-1999  
C;Accession: JN0724  
R;Huether, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.  
Gene 129, 285-289, 1993  
A;Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 beta  
A;Reference number: JN0724; MUID:93314975  
A;Molecule type: mRNA  
A;Residues: 1-267 <HUE>  
A;Cross-references: GB:M86725; NID:g164607; PIDN:AAA02584.1; PID:g164608  
A;Experimental source: alveolar macrophage  
C;Comment: This protein is a pleiotropic cytokine that mediates a variety of processes in  
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage  
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1  
C;Superfamily: interleukin-1  
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag  
F;115-267/product: interleukin-1 beta #status predicted <IL1>  
F;77/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 10.1%; Score 82; DB 1; Length 267;  
Best Local Similarity 26.1%; Pred. No. 3.2; Mismatches 31; Indels 12; Gaps 5;  
Matches 23; Conservative 22; Mismatches 31; Indels 12; Gaps 5;

Qy 4.9 YMYKDSEVRLAVTLSVKDSKXSTLSCKNK---IISFEEMDP---PENIDDIOSDLIFF 101  
Db 160 FVQGDDSNKIPVTLGIK-GKNLYLSCVMKDNTPTLQEDIDPKRYPR- -DMEKRFVFY 216

Qy 102 QKRVGEHKMEFESSLYVEGHFLACQKED 129  
Db 217 KTEI-KNRVEFESALYPNWVISTSQAE 242

RESULT 4

T21327 hypothetical protein F25C8.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T21327  
R;Matthews, L.  
Submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19407  
A;Accession: T21327  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Residues: 1-483 <WIL>  
A;Cross-references: EMBL:Z81512; PIDN:CAB04171.1; GSPDB:GN00023; CESP:F25C8.2  
A;Experimental source: clone F25C8  
C;Genetics:  
A;Gene: CESP:F25C8.2  
A;Map Position: 5  
A;Introns: 13/2; 136/2; 209/3; 358/3; 444/2

Query Match 10.0%; Score 81; DB 2; Length 483;  
Best Local Similarity 26.4%; Pred. No. 7.8; Mismatches 63; Indels 66; Gaps 12;  
Matches 55; Conservative 24; Mismatches 63; Indels 66; Gaps 12;

Qy 3 GRLHCTTAVIRNINDQV-----LFVDKRQPVFEDMTDIDQSAS----EPOTRLIIT 48  
Db 81 GYLHFGAEVNGVVDNEVYNVILVERKYDLF-DRTKPRTDLWMLDQDNISITLVNGLVPKIL 139

Qy 49 YMVKDSEVRLAVTLSVKDSKXSTLSCKNKIIS-FEEM- DPENIDDIOSDLIFFQKRV 105  
Db 140 DKFND-YIRYLNVALYEKSIKINOLSVENNEINNOQFIEFLRDVPENDHEIYESLINVK- 196

Qy 106 PGHNKMEFESSLYVEGHFL-----ACQKEDDA-----FKLILK----- 137  
Db 197 ---NYFQTEWSSPVGELSNSLIWDDGTEEEDSAFLNQGFYEILKDFRSKIPAGNIRL 253

Qy 138 -----KKDENGDKSVMFTLTN---LH 155  
Db 254 NCEVINKEEEN---IMVTLKNGEVLH 277

RESULT 5

S38373 interleukin-1 beta precursor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 20-May-1994 #sequence\_revision 01-Dec-1995 #text\_change 16-Jul-1999  
C;Accession: S38373  
R;Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; O  
Eur. J. Biochem. 217, 45-52, 1993  
A;Title: Gene sequence, cDNA construction, expression in Escherichia coli and genetic  
A;Reference number: S38373; MUID:94039070  
A;Accession: S38373  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-267 <VAN>  
A;Cross-references: EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g407900  
C;Genetics:  
A;Introns: 16/2; 33/3; 99/1; 154/1; 197/3  
C;Superfamily: interleukin-1

Query Match 10.0%; Score 80.5; DB 2; Length 267;  
Best Local Similarity 28.6%; Pred. No. 4.3; Mismatches 22; Indels 13; Gaps 6;  
Matches 24; Conservative 22; Mismatches 25; Indels 13; Gaps 6;

Qy 53 DSEVRLAVTLSVKDSKXSTLSCKNK---IISFEEMDP---PENIDDIOSDLIFFQKRV 105  
Db 165 DSDDK-IPTVTLGIK-GKNLYLSCVMKDNTPTLQEDIDPKRYPR- -DMEKRFVFY 220

Qy 106 PGHNKMEFESSLYVEGHFLACQKED 129

Db	221 --KNYEFESALYLPNNY1STSQAE	242
RESULT	6	
D71461	hypothetical protein CT861 - Chlamydia trachomatis (serotype D, strain UW3/Cx)	
C;Species:	Chlamydia trachomatis	
C;Date:	13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999	
C;Accession:	D71461	
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998		
A;Title:	Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac	
A;Reference number:	A71570; MUID:99000809	
A;Accession:	D71461	
A;Status:	preliminary	
A;Molecule type:	DNA	
A;Residues:	1-506 <ARN>	
A;Cross-references:	GB:AE001359; GB:AE001273; PIDN:ACC68459.1; PID:9332933	
A;Experimental source:	serotype D, strain UW-3/Cx	
C;Genetics:		
A;Gene:	CT861	
Query Match	9.9%	Score 80; DB 2; Length 506;
Best Local Similarity	25.0%	Pred. No. 10; Mismatches 55; Indels 34; Gaps 7;
Matches	38;	Conservative 25; Mismatches 55; Indels 34; Gaps 7;
QY	1	NFGRHLCTTAVIRNINDQVLFVDKRQPVFEDMTIDQDQSASEPQTRLIYMYKDSEVRGLA 60
Db	63	SFSRILQPTTP-----KERILFFGS-SPSQLSQTVRTTSSPWN-----LFNSNQTRNST 111
QY	61	VTLVKDKSXSXSTLSCKN--KLISFEEMDPPEIDIQSDLIFFQKRVPGHNMKEFESSLY 118
Db	112	RKLSERKLHFSELSARDSTKPSSEPIKPSENL-----LHTPEHHK-ELFSSLK 159
QY	119	EGHFLACQKEDDAF-----KLILKKDE 141
Db	160	KDNLSPIMEEDSFAETESLEERLYTQKEE 191
RESULT	7	
A41698	cell division control protein cdc55 - yeast (Saccharomyces cerevisiae)	
N;Alternate names:	Protein G1345; protein YGL190c	
C;Species:	Saccharomyces cerevisiae	
C;Date:	30-Jun-1992 #sequence_revision 18-Sep-1992 #text_change 29-Oct-1999	
C;Accession:	A41698; S31274; S61128; S62055; S64207; S18513	
R;Healy, A.M.; Zolnierowicz, S.; Stapleton, A.E.; Goebel, M.; DePaoli-Roach, A.A.; Pringl Mol. Cell. Biol. 11, 5767-5780, 1991		
A;Title:	cDC55, a Saccharomyces cerevisiae gene involved in cellular morphogenesis: identity, reference number: A41698; MUID:92017858	
A;Accession:	A41698	
A;Molecule type:	DNA	
A;Residues:	1-526 <HEAL>	
A;Cross-references:	GB:M72716	
A;Note:	the authors translated the codon TAT for residue 116 as Val and CCT for residue R; Healy, A.M.; Zolnierowicz, S.; Stapleton, A.E.; Goebel, M.; Depaoli-Roach, A.A.; Pringl submitted to the EMBL Data Library, July 1991	
A;Reference number:	S31274	
A;Accession:	S31274	
A;Molecule type:	DNA	
A;Residues:	1-499, 'N', 501-526 <HEAL>	
A;Cross-references:	EMBL:M72716; NID:91171194; PIDN:AAA34482.1; PID:g171195	
R;Bertani, I.; Coglilevina, M.; Zaccaria, P.; Klima, R.; Bruschi, C.V.		
A;Description:	The sequence analysis of a 7.9 kb DNA fragment from the left arm of S.cer submitted to the EMBL Data Library, September 1995	
A;Reference number:	S61128	
A;Accession:	S61128	
A;Molecule type:	DNA	
A;Residues:	1-281 <BER>	
A;Cross-references:	EMBL:X91489; NID:91143557; PIDN:CAA62785.1; PID:e199121; PID:g114355	
R;Coglilevina, M.; Delneri, D.; Zaccaria, P.; Klima, R.; Bertani, I.; Bruschi, C.V.		
Query Match	9.7%	Score 78.5; DB 2; Length 1039;
Best Local Similarity	26.4%	Pred. No. 32; Mismatches 50; Indels 39; Gaps 5;
Matches	37;	Conservative 14; Mismatches 50; Indels 39; Gaps 5;
QY	31	DMDTIDQDQSASEPQTRLIY-----YKDSEVRGLAVTLSVKDSKXSTL 73
Db	374	DIGEIDEELDEEFLRAVYFDKLDDMREELKKAOYAEDILVGKA-----DSKVETL 428
QY	74	SCKNRIISFEEMDPPEIDIQSDLIFFQKRVPGHNMKEFESSLYEGHFLACQKEDDAF 133
Db	429	--KKILGLVLVTPEELPDEFKDLA-SOKAIVTEFKDTATVLYE-----K 471

QY	134	LILKKKDENGDKSVMFTLTLN	153	toxin, nontoxic component - Clostridium botulinum phage (type C)
C;Species: Clostridium botulinum phage				
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 08-Oct-1999				
C;Accession: JQ1467; PQ0297; S22165				
R;tsuzuki, K.; Kimura, K.; Fujii, N.; Yokosawa, N.; Oguma, K.				
Biochem. Biophys. Res. Commun. 183, 1273-1279, 1992				
A;Title: The complete nucleotide sequence of the gene coding for the nontoxic-nonhemagglutinating toxin, nontoxic component - Clostridium botulinum phage (type C)				
A;Reference number: JQ1467; MUID:92231894				
A;Accession: JQ1467				
A;Molecule type: DNA				
A;Residues: 1-1196 <TSU>				
A;Cross-references: EMBL:X62389; NID:g558175; PIDN:CAA44262.1; PID:g40389				
A;Experimental source: strain C-Stockholm				
A;Accession: PQ0297				
A;Molecule type: protein				
A;Residues: 1-20 <TS2>				
C;Comment: This nontoxic component is a constituent of 16S(500K) toxin with two other components				
RESULT 9				
Query Match 9.7%; Score 78; DB 2; Length 1196;				
Best Local Similarity 24.3%; Pred. No. 42;				
Matches 35; Conservative 23; Mismatches 58; Indels 28; Gaps 4;				
QY 35 IDQSQASEPQTLLIYMKDSEVRGLAV--TLSVKDSKKSTLCKNNKIISFEEMDPEN-- 90				
Db 965 ISISVDRLLQDQLLIFI-NDKNVANVSIDQILSIYSTNIISLVNKNNSIYVEELSVLDNP 1023				
QY 91 -----IDDIQSLIFFQKRVPGHNMKEFESSLYEGHFLACQKEDDAFK 133				
Db 1024 TSEEVIRNYFSYLDNSYIRDSSKSLSLEYNKNYQOLYNVFPETSLYE-----VNDDNNKY 1077				
QY 134 LILKKKDENGDKSVMFTLTLNQS 157				
Db 1078 LSLKNTDGINISSVVKFLINIDES 1101				
RESULT 10				
S46430 botulinum neurotoxin-associated protein ANTP-139 - Clostridium botulinum phage 1C (strain N;Alternate names: ANTP-139 protein				
C;Species: Clostridium botulinum phage 1C				
A;Variety: strain C-468				
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999				
C;Accession: S46430; S49106				
R;Hauser, D.; Eklund, M.W.; Boquet, P.; Popoff, M.R.				
Mol. Gen. Genet. 243, 631-640, 1994				
A;Title: Organization of the botulinum neurotoxin C1 gene and its associated non-toxic genes				
A;Reference number: S46426; MUID:94301293				
A;Accession: S46430				
A;Status: nucleic acid sequence not shown; translation not shown				
A;Molecule type: DNA				
A;Residues: 1-1196 <HAU>				
A;Cross-references: EMBL:X72793; NID:g516171; PIDN:CAA51312.1; PID:g516174				
A;Experimental source: strain C-468				
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993				
RESULT 11				
E71616 hypothetical protein PFB0365w - malaria parasite (Plasmodium falciparum)				
C;Species: Plasmodium falciparum				
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999				
C;Accession: E71616				
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.E.; Clayton, R.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, F.; Science 282, 1126-1132, 1998				
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.				
A;Residues: 1-1247 <GAR>				
A;Cross-references: GB:AE001390; GB:AE001362; NID:g3845164; PID:g3845165; TIGR:PFB0365w				
A;Experimental source: clone 3D7				
A;Genetics:				
C;Genetics:				
C;Gene: PFB0365w				
RESULT 12				
T30457 hypothetical protein ORF107 - Lymantria dispar nuclear polyhedrosis virus				
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV				
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999				
C;Accession: T30457				
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Fries, J.; Virology 253, 17-34, 1999				
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria dispar				
A;Reference number: Z20836; MUID:99124785				
A;Accession: T30457				
A;Status: preliminary; translated from GB/EMBL/DDJB				
A;Molecule type: DNA				
A;Residues: 1-366 <KUZ>				
A;Cross-references: EMBL:AF081810; PIDN: AAC70293.1				
Query Match 9.6%; Score 77.5; DB 2; Length 366;				
Best Local Similarity 22.2%; Pred. No. 12;				
Matches 34; Conservative 31; Mismatches 63; Indels 25; Gaps 6;				
QY 10 AVIRNINDQVLFDVKRQPVFEDMDTIDQSQASEPQTLLIYMKDSEVRGLAVTLSVKDSK 69				
Db 41 ALVLNL--WVY----PTDEDIYVDASKLPAFQSVLVRY---ELGDASETRVPKNT 90				
QY 70 XSTLSCKNNKIISFEEMDPENDD----IQSDLIFFQKRVPGHNMEEFESSLYEGHFLACQKEDDAFK 118				
QY 91 -----IDDIQSLIFFQKRVPGHNMEEFESSLYEGHFLACQKEDDAFK 133				



